

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 02:01:47 ; Search time 1635.59 Seconds
(without alignments)
3025.428 Million cell updates/sec

Title: US-10-814-858A-2
Perfect score: 130
Sequence: 1 tcatatatatagaagttc.....ttacatctagataaacaatg 130

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	48	36.9	654	9	CG206846
C 2	42.6	32.8	884	8	AZ679757
C 3	42.6	32.8	888	8	AZ550547
C 4	42.6	32.8	935	8	AZ684425
C 5	39.8	30.6	424	5	BP617758
C 6	39.8	30.6	1093	3	CR725951
C 7	39	30.0	490	8	AZ045132
C 8	38.8	29.8	821	8	BH249781
C 9	38.8	29.8	963	9	CNS03E20
C 10	38.2	29.4	523	1	AA846861
C 11	37.8	29.1	530	8	AZ522110
C 12	37.8	29.1	979	9	CNS04LX9
C 13	37.4	28.8	572	4	BJ485243
C 14	37.4	28.8	628	4	BJ389532
C 15	37.4	28.8	752	1	AV711184
C 16	37.2	28.6	917	9	CG953396
C 17	37	28.5	1067	9	CNS03BJM
C 18	36.6	28.2	502	4	BI440260
C 19	36.6	28.2	893	8	AZ534920
C 20	36.6	28.2	898	8	AZ692862
C 21	36.6	28.2	1198	3	CR697279
C 22	36.6	28.2	1273	3	CL649111
C 23	36.4	28.0	513	8	AZ239942
C 24	36.4	28.0	2689	9	AG390466

25	36.2	27.8	495	9	CR358331	CR358331 Arabidops
C 26	36.2	27.8	670	9	CE140833	CE140833 tigr-gss8
C 27	36.2	27.8	964	8	BZ695586	BZ695586 SP_BA006
C 28	36.2	27.8	1269	9	CG749985	CG749985 P044-2-F0
C 29	36.2	27.8	1616	9	CL647121	CL647121 CH213-131
C 30	36	27.7	183	6	CB101154	CB101154 K167C11.Y
C 31	36	27.7	261	6	CA802634	CA802634 sau39G05
C 32	36	27.7	284	2	AW423991	AW423991 sh59b04.Y
C 33	36	27.7	522	8	AQ248025	AQ248025 HS_2015.A
C 34	36	27.7	681	1	AV317591	AV317591 AV317591
C 35	36	27.7	700	4	BG56147	BG56147 1024044G0
C 36	36	27.7	707	8	BH927322	BH927322 oeh93e02
C 37	36	27.7	751	8	BH736173	BH736173 BOH083TF
C 38	36	27.7	892	8	AZ686660	AZ686660 ENT081TF
C 39	36	27.7	905	9	CG438011	CG438011 OGTBK39TV
C 40	36	27.7	1032	9	CNS020IP	AL206746 Tetraodon
C 41	36	27.7	1525	9	AG486059	AG486059 Mus muscu
C 42	35.8	27.5	397	8	AQ102186	AQ102186 HS_3035.A
C 43	35.8	27.5	420	5	BQ584505	BQ584505 E011861-0
C 44	35.8	27.5	538	7	CF755575	CF755575 lae43b11
C 45	35.8	27.5	562	5	BP121578	BP121578 BP121578

ALIGNMENTS

RESULT 1
CG206846/c

LOCUS
DEFINITION

CG206846
CG206846

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

654 bp DNA linear GSS 21-AUG-2003
TOS0467 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza sativa (japonica cultivar-group) genomic clone TOSJNBH019110h, genomic survey sequence.
CG206846
CG206846.1 GI:34097907
GSS.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 654)
Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
BAC end sequences to close the gaps of a rice physical map at TAMU Unpublished (2003)
Contact: Wu C
Department of Soil and Crop Sciences and Institute for Plant Genomics and Biotechnology
Texas A & M University
TAMU 2474, College Station, TX 77843-2474, USA
Tel: 979 862 4800
Fax: 979 862 4790
Email: c-wu@neo.tamu.edu
Seq primer: MJ3 universal Forward GTAAACGACGGCCAGT
Class: BAC ends
High quality sequence stop: 654.
Location/Qualifiers
1. .654
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="TOSJNBH019110h"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/clone_lib="TAMU Rice Japonica Nipponbare BAC Library (Hind III)"
/note="Vector: V41"

FEATURES
source

Query Match 36.9%; Score 48; DB 9; Length 654;
Best Local Similarity 90.0%; Pred. No. 0.34;
Matches 63; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy	45	TGTCATTTCTCAACATTACCAGAACAAACAACAACATTTATACAATTACTAT	104
Dβ	156	TCATTTTTTACAAACAATTACCAACACAAACAAACAACAACAT--TACAATTACTAT	99
Qy	105	TTACAATTAC	114
Dβ	98	TTACAATTAC	89

RESULT 2
A2679757/c
LOCUS
DEFINITION
A2679757
ENTU131FF Entamoeba histolytica 884 bp DNA
genomic, genomic survey sequence.
ACCESSION
A2679757
VERSION
A2679757.1 GI:11816903
KEYWORDS
GSS.
SOURCE
Entamoeba histolytica
Entamoeba histolytica
ORGANISM
Eukaryota; Entamoebidae; Entamoeba.
REFERENCE
1 (bases 1 to 884)
Loftus, B., Van Aken, S. and Fraser, C.
AUTHORS
Determination of clone end sequences from Entamoeba histolytica
TITLE
HMI-1GSS sheared DNA library
JOURNAL
Unpublished (2000)
COMMENT
Contract: Brand

Dr. Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM:1MS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 15
High quality sequence stop: 806.
Location/Qualifiers

location/Qualifiers
1. .884
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS3; Site 1: Bat I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Batell, Oxford University Press, 1999)."

	Query Match	32.8;	Score 42.6;	DB 8;	Length 884;
	Best Local Similarity	61.1;	Pred. No. 5.9;		
	Matches	69;	Conservative	0;	Mismatches 44;
				Indels	0;
				Gaps	0;
Qy	18	TTCAATTCATTTGGAAATGGACAGCTGTGTGTCATTTCTCAACAATTCACCAACAACACACAA	77		
Db	551	TTTATTTTCATATATCTCTCTATCACTAATCTAAATTTAGCAATCTAATCAAAACAGTAAA	492		
Qy	78	CAACAAACAACATTATACAATTTACTATTTTACATTTACATCTAGATAAACAATG	130		
Db	491	CAACAAAATAATATTTTAAAGGAAATTAATACAAAGAAATTTGTAATTTAAATAATG	439		

RESULT 3	
AZ550547/C	
LOCUS	
DEFINITION	

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

[illegible]

FEATURES source

ORIGIN

Best Local
Matches 6

RESULT 4
584425/c

STATUS	A2
DEFINITION	EN
	G6
SESSION	A2
SESSION	A2
WORDS	G5
FORCE	EN

AZ550547 Entamoeba histolytica linear DNA 888 bp
Entamoeba histolytica Sheared genomic, genomic survey sequence.
GSS 14-NOV-2000

AZ550547.1 GR:11175848
GSS.
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae;
1 (bases 1 to 888)
Loft

Petrus, B., van Aken, S. and Fraser, C.
 Determination of clone end sequences from *Entamoeba histolytica*
 HM1:IMSS sheared DNA library
 Unpublished (2000)
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543

Email: Djlotus@tigr.org
 Genomes are derived from the Entamoeba histolytica HM1:IMSS sheared
 DNA library
 Sequenced by: M3-Forward
 Sequencing method: shotgun
 High quality sequence start: 16
 High quality sequence stop: 863.
 Localism/Qualifiers
 1 888

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/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_libs="Entamoeba histolytica Sheared DNA"
/notes="vector: pHOS1; Site 1; Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barell, Oxford University Press, 1993, pp. 11-18)."

```

32.8%; Score 42.6; DB 8; Length 888;
 Similarity 61.1%; Pred. No. 5.9;
 ; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 TTCAATTCATTGGGAATGGACACGCTGTGTCATTTCTCAACAATTTACCAACAACAACAAA 77
 TTTATTTCAATATATCTCTATCAACTAAATCTAATTTAGCAAACTCTAATCAAAAAACAGTAAA 251
 CAACAAAACAACATTATACAATTTACTATTTTACAAATTTACATCTAGATTAACAATG 130
 CAACAAAATAATTTTAAAGGAATTAATCAAGAATTTGTAATTTAAATATG 198

884425
PHS99TR Entamoeba histolytica
omic, genomic survey sequence.
884425
884425.1 GI:11821571
amoeba histolytica

```

TITLE      Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL    Science 296 (5565), 141-145 (2002)
MEDLINE    21932900
PUBMED     11910074
COMMENT    Contact: Motoaki Seki
           Plant Functional Genomics Research Group
           RIKEN Genomic Sciences Center
           3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
           Tel: 81-298-36-4359
           Fax: 81-298-36-9060
           Email: mseki@rtc.riken.go.jp
           reversed clone; Please visit our web site
           (http://pfweb.gsc.riken.go.jp/) for further details.
FEATURES   Location/Qualifiers
            source            1..424
                               /organism="Arabidopsis thaliana"
                               /mol_type="mRNA"
                               /db_xref="taxon:3702"
                               /clone="RAFL16-25-F22"
                               /lab_host="DH10B"
                               /clone_lib="RAFL16"
                               /notes="Site_1: BamHI; Site_2: SalI; dark-grown"
ORIGIN
Query Match      30.6%; Score 39.8; DB 5; Length 424;
Best Local Similarity 59.1%; Pred. No. 27;
Matches 68; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY      15  AAGTTCATTTTCATTTCGATGGACACGTCGTCTTCTTCTCAACAATTTACCAACAACAC 74
Ddb      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      34  ATGTTTCATATCATTAAGAGTAAATCAGAGTTTTCATTTTCACAGCAATTTCCATCGAAG 93
Ddb      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      75  AAACAACAACAACATTTATACAATTTACTATTATTCACATTTACATCTAGATAAAACAAT 129
Ddb      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      94  AATAGTAAACAAGTAAAGGTAACACATCACCCTAAAGGCAAT 148
Ddb      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
LOCUS      CR725951                1093 bp    mRNA    linear    HTC 19-AUG-2004
DEFINITION Tetraodon nigroviridis full-length cDNA.
ACCESSION  CR725951
VERSION    CR725951.1    GI:51224202
KEYWORDS   HTC; cDNA; full-length; Tetraodon nigroviridis.
SOURCE     Tetraodon nigroviridis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
           Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
           Tetraodontidae; Tetraodon.
REFERENCE  1  (bases 1 to 1093)
           Genoscope.
AUTHORS    Direct Submission
JOURNAL    Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
           : 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
           (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT    The sequences are based on single pass reads.
           More information available at
           http://www.genoscope.cns.fr/tetraodon.
FEATURES   Location/Qualifiers
            source            1..1093
                               /organism="Tetraodon nigroviridis"
                               /mol_type="mRNA"
                               /db_xref="taxon:99883"
                               /tissue_type="fish"
ORIGIN
Query Match      30.6%; Score 39.8; DB 3; Length 1093;
Best Local Similarity 57.7%; Pred. No. 26;
Matches 71; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY      5  TATATATPAGGAAGTTCATTTTCATTTGGAAATGGACACGTTGTGTCATTTTCAACAATTAC 64

```

Db 483 TATTTAAAGTGAATACATTTGTTTGTAGTAGACAAGTCTGAACTTGCAAAAGTAACAC 424
 QY 65 CAACAACACAAACAAACAAACATTTATATACAAATTTACTATTACAAATTCATCTAGATAA 124
 Db 423 CAAATATAGAAACCACTTAAATAAAGATGCCTCAAAATCTACAAATATTTCCAAATA 364
 QY 125 ACA 127
 Db 363 AAA 361

RESULT 7
 A2045132
 LOCUS
 DEFINITION Gm_UMB001_025_G19F UMN Soybean BAC Library GSS 31-JAN-2003
 max genomic clone Glycine max genomic clone Gm_UMB001_025_G19,
 genomic survey sequence.

ACCESSION
 VERSION A2045132
 KEYWORDS
 SOURCE GSS
 ORGANISM Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE
 AUTHORS Larson, K., Mudge, J., Cooper, A., Grivna, S., Denny, R., Penuela, S.,
 Danesh, D. and Young, N.D.
 TITLE BAC End sequences from a soybean genomic library (UMN)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Young Nevin D
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
 Tel: 612 625 2225
 Fax: 612 625 9728
 Email: nevin@c.umn.edu

Sequence on contig Gm_A963.ctg a near mapped duplicate of RFLP
 probe pA963 on linkage group F. For more information, see Soybase
 at: <http://soybase.agron.iastate.edu>. Please see as an authority
 for the mapping/naming: Cregan P.B., T. Jarvik, A.L. Bush, R.C.
 Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. Vantoi, D.G.
 Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic
 linkage map of the soybean genome. Crop Sci. 39:1464-1490
 Seq primer: M13F
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..490
 /organism="Glycine max"
 /mol_type="genomic DNA"
 /cultivar="Faribault"
 /db_xref="taxon:3847"
 /clone="Gm_UMB001_025_G19"
 /tissue_type="cotyledon leaves"
 /dev_stage="cotyledon"
 /clone_lib="UMN Soybean BAC Library (pEC5BAC4 EcoRI)"
 /note="Vector: pEC5BAC4; The UMN BAC library (Danesh et
 al, Theor. Appl. Genet. 96:196, 1998), was constructed
 using the Eco RI site of pEC5BAC4. The library consists
 of 72,960 clones with an average insert size of 120 kb.
 equal to 7 haploid genome equivalents. Screening of the
 library is done by hybridization of high-density colony
 filters and/or PCR amplification of DNA pools. Four high
 density filters, each containing 18,432 clones (doubly
 spotted), represent the whole library for colony
 screening"

ORIGIN

Query Match 30.0%; Score 39; DB 8; Length 490;
 Best Local Similarity 55.6%; Pred. No. 40;
 Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 5 TATATATAGGAAGTTCATTTTCATTTGGAAATGGACACGTGTGTTCATTTCTCAACAATTAC 64
 Db 250 TATATATATGACATAATTTTCTGGGTAGCGANNNGTGTGACAACTTGCACCACTAT 309
 QY 65 CAACAACACAAACAAACAAACATTTATACAAATTTACTATTACAAATTCATCTAGATAA 124
 Db 310 CTACCATATAGACAGAAAAAAGATTGAAATTTACAATCTAAATNNAATAACAAA 369
 QY 125 ACAA 128
 Db 370 ATAA 373

RESULT 8
 BH249781
 LOCUS

DEFINITION BH249781 821 bp DNA linear GSS 26-NOV-2001
 BOGAY07TF BOGA Brassica oleracea genomic clone BOGAY07, genomic
 survey sequence.

ACCESSION
 VERSION BH249781
 KEYWORDS
 SOURCE GSS
 ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
 AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished (2001)
 COMMENT Other GSSs: BOGAY07TR
 Contact: Chris Town
 TIGR

712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..821
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOGAY07"
 /clone_lib="BOGA"
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 29.8%; Score 38.8; DB 8; Length 821;
 Best Local Similarity 57.4%; Pred. No. 44;
 Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 7 TATATAGGAAGTTCATTTTCATTTGGAAATGGACACGTGTGTTCATTTCTCAACAATTACCA 66
 Db 307 TAAATAGGTCGTACATTTAGCTATGAATTTACTCTTTTATTATTACAGAAATTAATA 366
 QY 67 ACAACAACAACAACAACAACATTTATACAAATTTACTATTACAAATTCATCTAGATAAC 126
 Db 367 ATATAATTTAAAAAATACATAAATTTATTATTATTAAATAAATTAATTTAAATAA 426
 QY 127 AA 128
 Db 427 AA 428

RESULT 9
 CNS03E20/c
 LOCUS

CNS03E20 963 bp DNA linear GSS 01-SEP-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone sequence of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL241029

VERSION AL241029.1 GI:7961798

KEYWORDS GSS: genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis

DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1

AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W., and Weissenbach, J.

TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633

PUBMED 10835645

REFERENCE 2

AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE 20359837

PUBMED 10899143

REFERENCE 3 (bases 1 to 963)

AUTHORS Direct Submission

TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

JOURNAL This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source Location/Qualifiers

1..963

/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/db_xref="taxon:99883"

/clone="021G13"

/clone_lib="G"

/notes="Genoscope sequence ID : COBG021AD07LP1-end : T7"

ORIGIN

Query Match 29.8%; Score 38.8; DB 9; Length 963;

Best Local Similarity 69.3%; Pred. No. 44;

Matches 52; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 55 CAACAATTACCAACAACAACAACAACAATTATACATTATACATTATTTACAAATTAC 114

|||||

Db 298 CAACAACAACAACAACAACAACAACAACAACAACAATTCTTATTACTATTATATAT 239

QY 115 ATCTAGTAACAAAT 129

Db 238 AATWATAATAATAAT 224

RESULT 10

AA846861

LOCUS aa42c11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1392980

DEFINITION 3' similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AA846861

VERSION AA846861.1 GI:2933001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 523)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 446.

FEATURES

source Location/Qualifiers

1..523

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1392980"

/sex="male"

/lab host="DH10B"

/clone_lib="Soares testis NHT"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match 29.4%; Score 38.2; DB 1; Length 523;

Best Local Similarity 59.8%; Pred. No. 61;

Matches 64; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 21 ATTTCTTTTGGATGACACAGCTGTTCTCAATTTCTCAACAATTACCAACAACAACAACA 80

|||||

Db 237 AATTCATTTTGCATTTACAGCAGTTATATTTGTAGGAATGAAAACCAATGCATATA 296

QY 81 CAAACAACATTATACAAATTACTATTATTTACAAATTACATCTAGATAAACA 127

|||||

Db 297 AAACCAAAATGAAGAAAAAATAAGTTAGGCTTATATTATTATTACTCA 343

RESULT 11

AZ522110/C

LOCUS 202PbC04 Pb MEN #21 Plasmodium berghei genomic 3', genomic survey sequence.

DEFINITION AZ522110 530 bp DNA linear GSS 07-MAY-2001

ACCESSION AZ522110

VERSION AZ522110.1 GI:13960021

KEYWORDS GSS.

SOURCE Plasmodium berghei

ORGANISM Plasmodium berghei

DEFINITION Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 530)

AUTHORS Carlton, J.M.-R. and Dame, J.B.

TITLE The Plasmodium vivax and P. berghei gene sequence tag projects Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)

JOURNAL Contact: Dame JB

COMMENT Dept. of Pathobiology, College of Veterinary Medicine University of Florida 2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA Tel: 352 392 4700

/organism="Hordeum vulgare subsp. spontaneum"

FEATURES

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location/Quali
1. .572
/organism="Hor
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